

(FILE 'HOME' ENTERED AT 15:42:34 ON 25 APR 2003)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
ENTERED AT 15:43:02 ON 25 APR 2003

L1 2199 S SHOSHAN A?/AU OR WASSERMAN A?/AU OR MINTZ E?/AU OR MINTZ
L?/A
L2 17 S L1 AND TRANSCRIPTOME#
L3 6 DUP REM L2 (11 DUPLICATES REMOVED)
L4 2405 S TRANSCRIPTOME#
L5 14 S L4 AND (SPLIC? VARIANT#)
L6 60 S L4 AND MRNA TRANSCRIPT#
L7 306 S L4 AND LIBRAR###
L8 44 S L7 AND MICROARRAY
L9 0 S L4 AND OLGIONUCLEOTIDES
L10 7 DUP REM L5 (7 DUPLICATES REMOVED)
L11 14 DUP REM L6 (46 DUPLICATES REMOVED)
L12 25 DUP REM L8 (19 DUPLICATES REMOVED)
L13 6 S (L10 OR L11) AND (MICROARRAY OR CHIP OR GLASS SUPPORT)

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BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:519168 BIOSIS
 DOCUMENT NUMBER: PREV200100519168
 TITLE: DNA chips designed to detect alternative splicing using
 LEADS.
 AUTHOR(S): Wasserman, Alon (1); Shoshan, Avi (1); Grebinskiy,
 Vladimir
 (1)
 CORPORATE SOURCE: (1) Compugen Inc., Jamesburg, NJ USA
 SOURCE: International Genome Sequencing and Analysis Conference,
 (2000) Vol. 12, pp. 63. print.
 Meeting Info.: 12th International Genome Sequencing and
 Analysis Conference Miami Beach, Florida, USA September
 12-15, 2000
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English
 AB We design chips enabling the detection of alternative **splice**
variants. The design optimally chooses segments representing the
splice variants of each gene. Probes are selected from
 each segment using criteria including specificity, distance from the 3'
 end, sequence quality, GC content, and so on. The designs are based on
 the
 LEADS software that clusters and assembles ESTs, known mRNAs and genomic
 data. For each gene, it produces a list of predicted **mRNA**
transcripts, each a different **splice variant**.
 Multiply covered areas are used to detect and eliminate sequencing
 errors.
 These areas are also used for the detection of polymorphisms, which can
 be
 used in genotyping chips. Having good designs is crucial to extract
 meaningful information from **chip** experiments. Designs not using
 all available data, **splice variants** and sequencing
 errors might lead to useless probes and misleading results. It is
 believed
 that at least 35% of human genes have alternative **splice**
variants, and it is important to distinguish between their
 expression patterns. This is achieved by choosing probes that are unique
 to some of the variants. If one just wishes to measure the overall
 expression level of the gene, probes that are common to all the variants
 can be chosen.

138:164702

TITLE: Method and system for identifying **splice variants** of a gene
INVENTOR(S): Bingham, Jonathan; Srinivasan, Subha
PATENT ASSIGNEE(S): Jivan Biologics, Inc., USA
SOURCE: PCT Int. Appl., 28 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003014295	A2	20030220	WO 2002-US23819	20020725
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:			US 2001-307911P	P 20010725
			US 2001-329914P	P 20011017
			US 2001-343269P	P 20011221
			US 2001-343286P	P 20011221
			US 2001-343298P	P 20011221
			US 2002-146720	A 20020514

AB A method and system for identifying mRNA present in a sample. A **splice variant** technique selects a set of possible exon-exon junctions based on exons of expected **mRNA transcripts**. The **splice variant** technique then selects indicator polynucleotides for the exon-exon junctions and detects the expression level of the indicator polynucleotides in the sample. The **splice variant** technique then may use a math. algorithm to identify possible **splice variants** in the sample from the obsd. expression levels. The math. algorithm may be an algorithm for solving linear equations, a least squares algorithm, or any other algorithm for finding a possible soln. for a set of equations. The **splice variant** technique may also detect the expression levels of the exons themselves to provide more information for use in identifying the **splice variants** in the sample. The **splice variant** technique detects the expression levels of the exons by selecting indicator polynucleotides for the exons and designing probes to detect the expression level of the indicator polynucleotides (and thus the exons themselves) in the sample using the nucleotide array technol.

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L1      2199 S SHOSHAN A?/AU OR WASSERMAN A?/AU OR MINTZ E?/AU OR MINTZ
L?/A
L2      17 S L1 AND TRANSCRIPTOME#
L3      6 DUP REM L2 (11 DUPLICATES REMOVED)
L4      2405 S TRANSCRIPTOME#
L5      14 S L4 AND (SPLIC? VARIANT#)
L6      60 S L4 AND MRNA TRANSCRIPT#
L7      306 S L4 AND LIBRAR###
L8      44 S L7 AND MICROARRAY
L9      0 S L4 AND OLGIONUCLEOTIDES
L10     7 DUP REM L5 (7 DUPLICATES REMOVED)
L11     14 DUP REM L6 (46 DUPLICATES REMOVED)
L12     25 DUP REM L8 (19 DUPLICATES REMOVED)
L13     6 S (L10 OR L11) AND (MICROARRAY OR CHIP OR GLASS SUPPORT)
L14     21275 S MRNA TRANSCRIPT#
L15     311 S L14 AND SPLICE VARIANT#
L16     35 S L15 AND (OLIGONUCLEOTIDE LIBRAR### OR LIBRAR###)
L17     7 S L15 AND (MICROARRAY OR CHIP OR GLASS SUPPORT)
L18     14 DUP REM L16 (21 DUPLICATES REMOVED)
L19     6 DUP REM L17 (1 DUPLICATE REMOVED)
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